

sites : 20 40 60
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :

sites : 80 100 120
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :

sites : 140 160 180
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :

sites : 200 220 240
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :

sites : 260 280 300
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :

sites : 320 340 360
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :

sites : 380 400 420
 HSCYPFLA_CYP3A6/7 :
 HSRYP3_CYP3A7 :
 HSP4503A4_CYP3A4 :
 S74699_CYP3A5 :
 S74700_CYP3A5 :



REPLACEMENT SHEET

11/15

FIG. 9a(continued 1).

CYP3A4, CYP3A5, CYP3A6/7

sites	*	440	*	460	*	480	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	CGGCGGGG	AA	TTGG	ATGCA	TCG	TAA	168
S74700_CYP3A5	AAATTCG	TAATGT	TCGGT	TTAGT	ATTTGTA	TAAGTA	332
	AAATTCG	TAATGT	TCGGT	TTAGT	ATTTGTA	TAAGTA	477
sites	*	500	*	520	*	540	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	AGGCA	TTG	GGGTA	AGG	CA	ATG	207
S74700_CYP3A5	AAATTCG	TAATGT	TCGGT	TTAGT	ATTTGTA	TAAGTA	391
	AAATTCG	TAATGT	TCGGT	TTAGT	ATTTGTA	TAAGTA	537
sites	*	560	*	580	*	600	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	AT--	ATAT	AT	AT	AT	AT	255
S74700_CYP3A5	GTTCGGT	AT	AT	AT	AT	AT	450
	GTTCGGT	AT	AT	AT	AT	AT	597
sites	*	620	*	640	*	660	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	GGTATGT	TT	ATG	ATG	ATG	ATG	303
S74700_CYP3A5	G-TAGT	TT	ATG	ATG	ATG	ATG	508
	G-TAGT	TT	ATG	ATG	ATG	ATG	656
sites	*	680	*	700	*	720	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	AGT	AG	AG	AG	AG	AG	349
S74700_CYP3A5	AGT	AG	AG	AG	AG	AG	568
	AGT	AG	AG	AG	AG	AG	716
sites	*	740	*	760	*	780	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	TAATCA	TAAG	TAAG	TAAG	TAAG	TAAG	391
S74700_CYP3A5	TAATCA	TAAG	TAAG	TAAG	TAAG	TAAG	628
	TAATCA	TAAG	TAAG	TAAG	TAAG	TAAG	776
sites	*	800	*	820	*	840	
HSCYPFLA_CYP3A6/7	-----		-----		-----		-
HSRCYP3_CYP3A7	-----		-----		-----		-
HSP4503A4_CYP3A4	-----		-----		-----		-
S74699_CYP3A5	AGGCGG	AG	AG	AG	AG	AG	451
S74700_CYP3A5	AGGCGG	AG	AG	AG	AG	AG	688
	AGGCGG	AG	AG	AG	AG	AG	836



REPLACEMENT SHEET

12/15

FIG. 9a(Continued 2)

CYP3A4, CYP3A5, CYP3A6/7

sites	*	860	*	880	*	900	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	GTA AGA	TCGTGGCA	AGGG	ATCA	AGGG	TTG
S74699_CYP3A5	:	GTA AGA	TCGTGGCA	AGGG	ATCA	AGGG	TTG
S74700_CYP3A5	:	GTA AGA	TCGTGGCA	AGGG	ATCA	AGGG	TTG
	:						511
	:						747
	:						893
sites	*	920	*	940	*	960	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	569
S74699_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	807
S74700_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	950
sites	*	980	*	1000	*	1020	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	629
S74699_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	867
S74700_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1010
sites	*	1040	*	1060	*	1080	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	688
S74699_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	927
S74700_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1068
sites	*	1100	*	1120	*	1140	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	736
S74699_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	987
S74700_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1128
sites	*	1160	*	1180	*	1200	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	796
S74699_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1046
S74700_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1187
sites	*	1220	*	1240	*	1260	
HSCYPFLA_CYP3A6/7	:	-----	:	-----	:	-----	-
HSRCYP3_CYP3A7	:	-----	:	-----	:	-----	-
HSP4503A4_CYP3A4	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	856
S74699_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1105
S74700_CYP3A5	:	TCGTGGCA	AGGG	ATCA	AGGG	TTG	1247

[illegible]



REPLACEMENT SHEET

14/15

FIG. 9(b).

```
A or G
=
MEME repeated motif 9
=====
MEME 'single' motif 9
=====
Yi-consensus
=====
apoE-undefined-site-3
=====
ApoE_B1
=====
APRT-human_US
=====
APRT-CHO_US
=====
1238 AGCTGCAGCCCCACCTCCTTCTCCAGC
TCGACGTCGGGGTGGAGGAAGAGGTCG
```

(B) A

FIG. 9(c).

```
MEME repeated motif 2
=====
MEME repeated motif 2
=====
MEME 'single' motif 9
=====
Yi-consensus
=====
Sp1-TPI_(4)
=====
GCF-consensus
=====
DSE_(1)
=====
IRE_(1)
=====
Sp1_CS4
=====
GC-box_(1)
=====
Sp1-IE-4/5
=====
Sp1-IE-3.3
=====
E2A_CS hsp70.2
=====
E2A_CSSp1-hsp70_(1)
=====
APRT-mouse_US
=====
1379 AGCTGCAGCCCCGCCTCCTTCTCCAGC
TCGACGTCGGGGCGGAGGAAGAGGTCG
```

(B) G



REPLACEMENT SHEET

15/15

FIG. 9(d).

```
MEME repeated motif 9
=====
MEME repeated motif 9
=====
MEME repeated motif 3
=====
MEME 'single' motif 6
=====
E-2.7_kb_(3)
=
E1A-F_CS
=====
GH1          MTVGRE_NRS
=====
910 TCTGTCTGGCTGGGCTTGCAAGGATGTGTAG (A) T
    AGACAGACCGACCCGAACGTTCTACACATC
.....
```

FIG. 9(e).

```
MEME repeated motif 9
=====
MEME repeated motif 9
=====
MEME repeated motif 9
=====
MEME repeated motif 3
=====
MEME 'single' motif 6
=====
E-2.7_kb_(3)
=
MBF-I_CS
=====
E1A-F_CS
=====
CNBP-SREMTVGRE_NRS
=====
GH1          MRE_CS2
=====
1052 TCTGTCTGGCTGGGCTTGCAAGGATGTGTAG (A) G
    AGACAGACCGACCCGACGTTCTACACATC
.....
```